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TECH CENTER 1600/2900



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RAW SEQUENCE LISTING

DATE: 03/20/2003

PATENT APPLICATION: US/09/849,869A

TIME: 16:08:26

#24

Input Set : A:\CALTE.004C1 (CP1) revised.txt

Output Set: N:\CRF4\03202003\I849869A.raw

```

4 <110> APPLICANT: Anderson, David J.
5     Dong, Xinzhong
6     Zylka, Mark
7     Simon, Melvin
8     Han, Sang-kyou
10 <120> TITLE OF INVENTION: PAIN SIGNALING MOLECULES
13 <130> FILE REFERENCE: CALTE.004C1
15 <140> CURRENT APPLICATION NUMBER: US 09/849,869A
16 <141> CURRENT FILING DATE: 2001-05-04
18 <150> PRIOR APPLICATION NUMBER: US 60/222,344
19 <151> PRIOR FILING DATE: 2000-08-01
21 <150> PRIOR APPLICATION NUMBER: US 60/202,027
22 <151> PRIOR FILING DATE: 2000-05-04
24 <150> PRIOR APPLICATION NUMBER: US 09/704,707
25 <151> PRIOR FILING DATE: 2000-11-03
27 <150> PRIOR APPLICATION NUMBER: US 60/285,493
28 <151> PRIOR FILING DATE: 2001-04-19
30 <160> NUMBER OF SEQ ID NOS: 115
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1088
36 <212> TYPE: DNA
37 <213> ORGANISM: Mus Musculus
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (115)...(1026)
43 <400> SEQUENCE: 1
44 acagaagcca gagagctaca tccagcaaga ggaatggggg aaagcagcac ctgtgcaggg 60
45 tttctagccc taaacacatc ggcctcgcca acagcaccca caacaactaa tcca atg 117
46                                     Met
47                                     1
49 gac aat acc atc cct gga ggt atc aac atc acg att ctg atc cca aac 165
50 Asp Asn Thr Ile Pro Gly Gly Ile Asn Ile Thr Ile Leu Ile Pro Asn
51         5                10                15
53 ttg atg atc atc atc ttc gga ctg gtc ggg ctg aca gga aat ggc att 213
54 Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly Ile
55         20                25                30
57 gtg ttc tgg ctc ctg ggc ttc tgt ttg cac agg aac gcc ttc tca gtc 261
58 Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser Val
59         35                40                45
61 tac atc cta aac tta gct cta gct gac ttc ttc ctc cta ggt cac 309
62 Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly His
63 50                55                60                65

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65 atc ata gat tcc ata ctg ctt ctt ctc aat gtt ttc tac cca att acc 357
66 Ile Ile Asp Ser Ile Leu Leu Leu Leu Asn Val Phe Tyr Pro Ile Thr
67          70          75          80
69 ttt ctc ttg tgc ttt tac acg atc atg atg gtt ctc tat atc gca ggc 405
70 Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala Gly
71          85          90          95
73 ctg agc atg ctc agt gcc atc agc act gag cgc tgc ctg tct gta ctg 453
74 Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu
75          100          105          110
77 tgc ccc atc tgg tat cac tgt cac cgc cca gaa cac aca tca act gtc 501
78 Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr Val
79          115          120          125
81 atg tgt gct gtc atc tgg gtc ctg tcc ctg ttg atc tgc att ctg aat 549
82 Met Cys Ala Val Ile Trp Val Leu Ser Leu Ile Cys Ile Leu Asn
83 130          135          140          145
85 agt tat ttc tgc ggt ttc tta aat acc caa tat aaa aat gaa aat ggg 597
86 Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn Gly
87          150          155          160
89 tgt ctg gca ttg aac ttc ttt act gct gca tac ctg atg ttt ttg ttt 645
90 Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu Phe
91          165          170          175
93 gtg gtc ctc tgt ctg tcc agc ctg gct ctg gtg gcc agg ttg ttc tgt 693
94 Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe Cys
95          180          185          190
97 ggt act ggg cag ata aag ctt acc aga ttg tat gta acc att att ctg 741
98 Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile Leu
99          195          200          205
101 agc att ttg gtt ttt ctc ctt tgc gga ttg ccc ttt ggc atc cac tgg 789
102 Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His Trp
103 210          215          220          225
105 ttt ctg tta ttc aag att aag gat gat ttt cat gta ttt gat ctt gga 837
106 Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu Gly
107          230          235          240
109 ttt tat ctg gca tca gtt gtc ctg act gct att aat agc tgt gcc aac 885
110 Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala Asn
111          245          250          255
113 ccc atc att tac ttc ttc gtg gga tcc ttc agg cat cgg ttg aag cac 933
114 Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys His
115          260          265          270
117 cag acc ctc aaa atg gtt ctc cag aat gca ctg caa gac act cct gag 981
118 Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro Glu
119          275          280          285
121 aca gcc aaa atc atg gtg gag atg tca aga agc aaa tca gag cca 1026
122 Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
123 290          295          300
125 tgatgaagag cctttgctg gcccttagaa gtggctttgg ggtgagcatt gccctgctgc 1086
126 ac 1088
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 304

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130 <212> TYPE: PRT
131 <213> ORGANISM: Mus Musculus
133 <400> SEQUENCE: 2
134 Met Asp Asn Thr Ile Pro Gly Gly Ile Asn Ile Thr Ile Leu Ile Pro
135 1 5 10 15
136 Asn Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly
137 20 25 30
138 Ile Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser
139 35 40 45
140 Val Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly
141 50 55 60
142 His Ile Ile Asp Ser Ile Leu Leu Leu Asn Val Phe Tyr Pro Ile
143 65 70 75 80
144 Thr Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala
145 85 90 95
146 Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val
147 100 105 110
148 Leu Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr
149 115 120 125
150 Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile Leu
151 130 135 140
152 Asn Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn
153 145 150 155 160
154 Gly Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu
155 165 170 175
156 Phe Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe
157 180 185 190
158 Cys Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile
159 195 200 205
160 Leu Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His
161 210 215 220
162 Trp Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu
163 225 230 235 240
164 Gly Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala
165 245 250 255
166 Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys
167 260 265 270
168 His Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro
169 275 280 285
170 Glu Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
171 290 295 300
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 1234
176 <212> TYPE: DNA
177 <213> ORGANISM: Mus musculus
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (137)...(1051)
183 <400> SEQUENCE: 3

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184 tctgtagtga ctgtatcttt ccttctacac aagccagtga gctacatcca acaagaggat 60
185 tggggaaagc aatggtgaag catttcttgc cttaagacc tcagcctcac caacagcacc 120
186 agtgacaaca aatcca atg gac gaa acc ctc cct gga agt atc aac att agg 172
187 Met Asp Glu Thr Leu Pro Gly Ser Ile Asn Ile Arg
188 1 5 10
190 att ctg atc cca aaa ttg atg atc atc atc ttc gga ctg gtc gga ctg 220
191 Ile Leu Ile Pro Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu
192 15 20 25
194 atg gga aac gcc att gtg ttc tgg ctc ctg ggc ttc cac ttg cgc aag 268
195 Met Gly Asn Ala Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys
196 30 35 40
198 aat gac ttc tca ctc tac atc cta aac ttg gcc cgg gct gac ttc ctt 316
199 Asn Asp Phe Ser Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu
200 45 50 55 60
202 ttc ctc ctc agt agt atc ata gct tcc acc ctg ttt ctt ctc aaa gtt 364
203 Phe Leu Leu Ser Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val
204 65 70 75
206 tcc tac ctc agc atc atc ttt cac ttg tgc ttt aac acc att atg atg 412
207 Ser Tyr Leu Ser Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met
208 80 85 90
210 gtt gtc tac atc aca ggg ata agc atg ctc agt gcc atc agc act gag 460
211 Val Val Tyr Ile Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu
212 95 100 105
214 tgc tgc ctg tct gtc ctg tgc ccc acc tgg tat cgc tgc cac cgt cca 508
215 Cys Cys Leu Ser Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro
216 110 115 120
218 gta cat aca tca act gtc atg tgt gct gtg atc tgg gtc cta tcc ctg 556
219 Val His Thr Ser Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu
220 125 130 135 140
222 ttg atc tgc att ctg aat agc tat ttc tgt gct gtc tta cat acc aga 604
223 Leu Ile Cys Ile Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg
224 145 150 155
226 tat gat aat gac aat gag tgt ctg gca act aac atc ttt acc gcc tcg 652
227 Tyr Asp Asn Asp Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser
228 160 165 170
230 tac atg ata ttt ttg ctt gtg gtc ctc tgt ctg tcc agc ctg gct ctg 700
231 Tyr Met Ile Phe Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu
232 175 180 185
234 ctg gcc agg ttg ttc tgt ggc gct ggg cag atg aag ctt acc aga ttt 748
235 Leu Ala Arg Leu Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe
236 190 195 200
238 cat gtg acc atc ttg ctg acc ctt ttg gtt ttt ctc ctc tgc ggg ttg 796
239 His Val Thr Ile Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu
240 205 210 215 220
242 ccc ttt gtc atc tac tgc atc ctg tta ttc aag att aag gat gat ttc 844
243 Pro Phe Val Ile Tyr Cys Ile Leu Leu Phe Lys Ile Lys Asp Asp Phe
244 225 230 235
246 cat gta tta gat gtt aat ttt tat cta gca tta gaa gtc ctg act gct 892
247 His Val Leu Asp Val Asn Phe Tyr Leu Ala Leu Glu Val Leu Thr Ala

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248          240          245          250
250 att aac agc tgt gcc aac ccc atc atc tac ttc ttc gtg ggc tct ttc 940
251 Ile Asn Ser Cys Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
252          255          260          265
254 aga cat cag ttg aag cac cag acc ctc aaa atg gtt ctc cag agt gca 988
255 Arg His Gln Leu Lys His Gln Thr Leu Lys Met Val Leu Gln Ser Ala
256          270          275          280
258 ctg cag gac act cct gag aca gct gaa aac atg gta gag atg tca agt 1036
259 Leu Gln Asp Thr Pro Glu Thr Ala Glu Asn Met Val Glu Met Ser Ser
260 285          290          295          300
262 aac aaa gca gag cct tgatgaagag cctctacctg gacctcagag gtggctttgg 1091
263 Asn Lys Ala Glu Pro
264          305
266 agtgagcact gccctgctgc acttgaccac tgtccactct tctctcagct tactgatttg 1151
267 acatgcctca gtggctccacc aacaacttca acatctctcc actaacttag ttttctacc 1211
268 cctcctgaat aaaagcatta atc 1234
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 305
272 <212> TYPE: PRT
273 <213> ORGANISM: Mus musculus
275 <400> SEQUENCE: 4
276 Met Asp Glu Thr Leu Pro Gly Ser Ile Asn Ile Arg Ile Leu Ile Pro
277 1          5          10          15
278 Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Met Gly Asn Ala
279          20          25          30
280 Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys Asn Asp Phe Ser
281          35          40          45
282 Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu Phe Leu Leu Ser
283          50          55          60
284 Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val Ser Tyr Leu Ser
285 65          70          75          80
286 Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met Val Val Tyr Ile
287          85          90          95
288 Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu Cys Cys Leu Ser
289          100          105          110
290 Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro Val His Thr Ser
291          115          120          125
292 Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile
293          130          135          140
294 Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg Tyr Asp Asn Asp
295 145          150          155          160
296 Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser Tyr Met Ile Phe
297          165          170          175
298 Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu Leu Ala Arg Leu
299          180          185          190
300 Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe His Val Thr Ile
301          195          200          205
302 Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Val Ile
303          210          215          220

```

VERIFICATION SUMMARY

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L:5310 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

L:5313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:114